

RAW SEQUENCE LISTING

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Application Serial Number: 09/868,533
Source: IFW/O
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IFWO

RAW SEQUENCE LISTING

DATE: 02/08/2006

PATENT APPLICATION: US/09/868,533

TIME: 12:04:20

Input Set : E:\pg3600 Seq Listing.txt

Output Set: N:\CRF4\02082006\I868533.raw

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4 <110> APPLICANT: Glaxo Group Limited
5     Farrow, Stuart N
6     Kaptein, Allard
7     Kitson, Jeremy DA
8     Winder, Alison J
10 <120> TITLE OF INVENTION: Novel Ligand
12 <130> FILE REFERENCE: PG3600
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/868,533
C--> 15 <141> CURRENT FILING DATE: 2001-06-19
17 <150> PRIOR APPLICATION NUMBER: GB 9828628.9
18 <151> PRIOR FILING DATE: 1998-12-23
20 <160> NUMBER OF SEQ ID NOS: 8
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 153
26 <212> TYPE: PRT
27 <213> ORGANISM: Homo sapiens
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30 Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln Asp Cys Leu Gln
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33 Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly Ser Tyr Thr
34           20           25           30
36 Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu Glu
37           35           40           45
39 Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe Ile Tyr
40           50           55           60
42 Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His Leu Ile
43   65           70           75           80
45 Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val Thr
46           85           90           95
48 Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn Asn Ser
49           100          105          110
51 Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Gly Leu Gln
52           115          120          125
54 Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp Val
55           130          135          140
57 Thr Phe Phe Gly Ala Leu Lys Leu Leu
58 145          150
60 <210> SEQ ID NO: 2
61 <211> LENGTH: 285
62 <212> TYPE: PRT
63 <213> ORGANISM: Homo sapiens
65 <400> SEQUENCE: 2

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66 Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu
67   1           5           10           15
69 Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
70           20           25           30
72 Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
73           35           40           45
75 Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
76           50           55           60
78 Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
79  65           70           75           80
81 Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
82           85           90           95
84 Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
85           100          105          110
87 Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
88           115          120          125
90 Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln
91           130          135          140
93 Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys
94 145          150          155          160
96 Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser
97           165          170          175
99 Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr
100          180          185          190
102 Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met
103          195          200          205
105 Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu
106          210          215          220
108 Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu
109 225          230          235          240
111 Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly
112          245          250          255
114 Asp Gly Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu
115          260          265          270
117 Asp Gly Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
118          275          280          285
123 <210> SEQ ID NO: 3
124 <211> LENGTH: 462
125 <212> TYPE: DNA
126 <213> ORGANISM: Homo sapiens
128 <220> FEATURE:
129 <221> NAME/KEY: CDS
130 <222> LOCATION: (1)..(462)
132 <400> SEQUENCE: 3
133 cgt gcc gtt cag ggt cca gaa gaa aca gtc act caa gac tgc ttg caa   48
134 Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln Asp Cys Leu Gln
135   1           5           10           15
137 ctg att gca gac agt gaa aca cca act ata caa aaa gga tct tac aca   96
138 Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly Ser Tyr Thr

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139          20          25          30
141 ttt gtt cca tgg ctt ctc agc ttt aaa agg gga agt gcc cta gaa gaa 144
142 Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu Glu
143          35          40          45
145 aaa gag aat aaa ata ttg gtc aaa gaa act ggt tac ttt ttt ata tat 192
146 Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe Ile Tyr
147          50          55          60
149 ggt cag gtt tta tat act gat aag acc tac gcc atg gga cat cta att 240
150 Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His Leu Ile
151 65          70          75          80
153 cag agg aag aag gtc cat gtc ttt ggg gat gaa ttg agt ctg gtg act 288
154 Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val Thr
155          85          90          95
157 ttg ttt cga tgt att caa aat atg cct gaa aca cta ccc aat aat tcc 336
158 Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn Asn Ser
159          100          105          110
161 tgc tat tca gct ggc att gca aaa ctg gaa gaa gga gat gga ctc caa 384
162 Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Gly Leu Gln
163          115          120          125
165 ctt gca ata cca aga gaa aat gca caa ata tca ctg gat gga gat gtc 432
166 Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp Val
167          130          135          140
169 aca ttt ttt ggt gca ttg aaa ctg ctg tga 462
170 Thr Phe Phe Gly Ala Leu Lys Leu Leu
171 145          150
174 <210> SEQ ID NO: 4
175 <211> LENGTH: 858
176 <212> TYPE: DNA
177 <213> ORGANISM: Homo sapiens
179 <220> FEATURE:
180 <221> NAME/KEY: CDS
181 <222> LOCATION: (1)..(858)
183 <400> SEQUENCE: 4
184 atg gat gac tcc aca gaa agg gag cag tca cgc ctt act tct tgc ctt 48
185 Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu
186 1          5          10          15
188 aag aaa aga gaa gaa atg aaa ctg aag gag tgt gtt tcc atc ctc cca 96
189 Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
190          20          25          30
192 cgg aag gaa agc ccc tct gtc cga tcc tcc aaa gac gga aag ctg ctg 144
193 Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
194          35          40          45
196 gct gca acc ttg ctg ctg gca ctg ctg tct tgc tgc ctc acg gtg gtg 192
197 Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
198          50          55          60
200 tct ttc tac cag gtg gcc gcc ctg caa ggg gac ctg gcc agc ctc cgg 240
201 Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
202 65          70          75          80
204 gca gag ctg cag ggc cac cac gcg gag aag ctg cca gca gga gca gga 288

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205 Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
206      85      90      95
208 gcc ccc aag gcc ggc ctg gag gaa gct cca gct gtc acc gcg gga ctg 336
209 Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
210      100      105      110
212 aaa atc ttt gaa cca cca gct cca gga gaa ggc aac tcc agt cag aac 384
213 Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
214      115      120      125
216 agc aga aat aag cgt gcc gtt cag ggt cca gaa gaa aca gtc act caa 432
217 Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln
218      130      135      140
220 gac tgc ttg caa ctg att gca gac agt gaa aca cca act ata caa aaa 480
221 Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys
222 145      150      155      160
224 gga tct tac aca ttt gtt cca tgg ctt ctc agc ttt aaa agg gga agt 528
225 Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser
226      165      170      175
228 gcc cta gaa gaa aaa gag aat aaa ata ttg gtc aaa gaa act ggt tac 576
229 Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr
230      180      185      190
232 ttt ttt ata tat ggt cag gtt tta tat act gat aag acc tac gcc atg 624
233 Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met
234      195      200      205
236 gga cat cta att cag agg aag aag gtc cat gtc ttt ggg gat gaa ttg 672
237 Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu
238      210      215      220
240 agt ctg gtg act ttg ttt cga tgt att caa aat atg cct gaa aca cta 720
241 Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu
242 225      230      235      240
244 ccc aat aat tcc tgc tat tca gct ggc att gca aaa ctg gaa gaa gga 768
245 Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly
246      245      250      255
248 gat gga ctc caa ctt gca ata cca aga gaa aat gca caa ata tca ctg 816
249 Asp Gly Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu
250      260      265      270
252 gat gga gat gtc aca ttt ttt ggt gca ttg aaa ctg ctg tga 858
253 Asp Gly Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
254      275      280      285
260 <210> SEQ ID NO: 5
261 <211> LENGTH: 144
262 <212> TYPE: PRT
263 <213> ORGANISM: Mus sp.
265 <400> SEQUENCE: 5
266 Ile Ile Gln Asp Cys Leu Gln Leu Ile Ala Asp Ser Asp Thr Pro Thr
267 1      5      10      15
269 Ile Arg Lys Gly Thr Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys
270      20      25      30
272 Arg Gly Asn Ala Leu Glu Glu Lys Glu Asn Lys Ile Val Val Arg Gln
273      35      40      45

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275 Thr Gly Tyr Phe Phe Ile Tyr Ser Gln Val Leu Tyr Thr Asp Pro Ile
276      50                      55                      60
278 Phe Ala Met Gly His Val Ile Gln Arg Lys Lys Val His Val Phe Gly
279 65                      70                      75                      80
281 Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro
282                      85                      90                      95
284 Lys Thr Leu Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Arg Leu
285                      100                     105                     110
287 Glu Glu Gly Asp Glu Ile Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln
288                      115                     120                     125
290 Ile Ser Arg Asn Gly Asp Asp Thr Phe Phe Gly Ala Leu Lys Leu Leu
291      130                      135                      140
294 <210> SEQ ID NO: 6
295 <211> LENGTH: 309
296 <212> TYPE: PRT
297 <213> ORGANISM: Mus sp.
299 <400> SEQUENCE: 6
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301 1      5                      10                      15
303 Ser Glu Lys Gly Glu Asp Met Lys Val Gly Tyr Asp Pro Ile Thr Pro
304      20                      25                      30
306 Gln Lys Glu Glu Gly Ala Trp Phe Gly Ile Cys Arg Asp Gly Arg Leu
307      35                      40                      45
309 Leu Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Ser Ser Phe Thr Ala
310      50                      55                      60
312 Met Ser Leu Tyr Gln Leu Ala Ala Leu Gln Ala Asp Leu Met Asn Leu
313 65                      70                      75                      80
315 Arg Met Glu Leu Gln Ser Tyr Arg Gly Ser Ala Thr Pro Ala Ala Ala
316      85                      90                      95
318 Gly Ala Pro Glu Leu Thr Ala Gly Val Lys Leu Leu Thr Pro Ala Ala
319      100                     105                     110
321 Pro Arg Pro His Asn Ser Ser Arg Gly His Arg Asn Arg Arg Ala Phe
322      115                     120                     125
324 Gln Gly Pro Glu Glu Thr Glu Gln Asp Val Asp Leu Ser Ala Pro Pro
325      130                     135                     140
327 Ala Pro Cys Leu Pro Gly Cys Arg His Ser Gln His Asp Asp Asn Gly
328 145                      150                      155                      160
330 Met Asn Leu Arg Asn Ile Ile Gln Asp Cys Leu Gln Leu Ile Ala Asp
331      165                      170                      175
333 Ser Asp Thr Pro Thr Ile Arg Lys Gly Thr Tyr Thr Phe Val Pro Trp
334      180                      185                      190
336 Leu Leu Ser Phe Lys Arg Gly Asn Ala Leu Glu Glu Lys Glu Asn Lys
337      195                      200                      205
339 Ile Val Val Arg Gln Thr Gly Tyr Phe Phe Ile Tyr Ser Gln Val Leu
340      210                      215                      220
342 Tyr Thr Asp Pro Ile Phe Ala Met Gly His Val Ile Gln Arg Lys Lys
343 225                      230                      235                      240
345 Val His Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys
346      245                      250                      255

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VERIFICATION SUMMARY

DATE: 02/08/2006

PATENT APPLICATION: US/09/868,533

TIME: 12:04:21

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L:14 M:270 C: Current Application Number differs, Replaced Current Application Number

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date